Figure 1A

```
1   ACAAATGACCGGGAGCCATGACGTCATCGGGGGCGCAGGAAAGCAGGTGCTCTGCTGCTT   60
1      M  T  G  S  H  D  V  I  G  G  A  G  K  Q  V  L  C  C  F     19

61  TTGCAAGCAGAGAAATAAGAGTTTGGGCACCTACCCAGGGGTCCCAGGGAATGCCCTGTG   120
20  C  K  Q  R  N  K  S  L  G  T  Y  P  G  V  P  G  N  A  L  W     39

121 GCTCCTGACCTCCCCCGCCTGTAATGCTCTGAGCACTTCAGCAGTAATGCATGGAAGAGA   180
40  L  L  T  S  P  A  C  N  A  L  S  T  S  A  V  M  H  G  R  D     59

181 TAAGGGGTCTGTGACCCATGGAACTGTCCAAGTCCTCTCTGACACCCGCTTCTTTTCCTG   240
60  K  G  S  V  T  H  G  T  V  Q  V  L  S  D  T  R  F  F  S  C     79

241 CCGTGAAGGACTACTTCCAGCAACCCAGTCTCCTGCCATGTCCGACCCCATCACGCTGAA   300
80  R  E  G  L  L  P  A  T  Q  S  P  A  M  S  D  P  I  T  L  N     99

301 CGTCGGGGGGAAGCTCTATACAACCTCACTGGCGACCCTGACCAGCTTCCCTGACTCCAT   360
100 V  G  G  K  L  Y  T  T  S  L  A  T  L  T  S  F  P  D  S  M     119

361 GCTAGGCGCCATGTTCAGCGGGAAGATGCCCACCAAGAGGGACAGCCAGGGCAACTGCTT   420
120 L  G  A  M  F  S  G  K  M  P  T  K  R  D  S  Q  G  N  C  F     139

421 CATTGACCGTGACGGCAAAGTGTTCCGCTATATCCTCAACTTCCTGCGGACCTCCCACCT   480
140 I  D  R  D  G  K  V  F  R  Y  I  L  N  F  L  R  T  S  H  L     159

481 TGACCTGCCTGAGGACTTCCAGGAGATGGGGCTGCTCCGCAGGGAGGCCGACTTCTACCA   540
160 D  L  P  E  D  F  Q  E  M  G  L  L  R  R  E  A  D  F  Y  Q     179

541 GGTGCAGCCCCTGATTGAGGCCCTGCAGGAGAAGGAAGTGGAGCTCTCCAAGGCCGAGAA   600
180 V  Q  P  L  I  E  A  L  Q  E  K  E  V  E  L  S  K  A  E  K     199

601 GAATGCCATGCTCAACATCACACTGAACCAGCGTGTGCAGACGGTCCACTTCACTGTGCG   660
200 N  A  M  L  N  I  T  L  N  Q  R  V  Q  T  V  H  F  T  V  R     219

661 CGAGGCACCCCAGATCTACAGCCTCTCCTCTTCCAGCATGGAGGTCTTCAACGCCAACAT   720
220 E  A  P  Q  I  Y  S  L  S  S  S  S  M  E  V  F  N  A  N  T     239

721 CTTCAGCACCTCCTGCCTCTTCCTCAAGCTCCTTGGCTCTAAGCTCTTCTACTGCTCCAA   780
240 F  S  T  S  C  L  F  L  K  L  L  G  S  K  L  F  Y  C  S  N     259

781 TGGCAATCTCTCCTCCATCACCAGCCACTTGCAGGACCCCAACCACCTGACTCTGGACTG   840
260 G  N  L  S  S  I  T  S  H  L  Q  D  P  N  H  L  T  L  D  W     279

841 GGTGGCCAATGTGGAGGGCCTGCCAGAGGAGGAGTACACCAAGCAGAACCTCAAGAGGCT   900
280 V  A  N  V  E  G  L  P  E  E  E  Y  T  K  Q  N  L  K  R  L     299
```

Figure 1B

```
901  CTGGGTGGTGCCCGCCAACAAGCAGATCAACAGCTTCCAGGTCTTCGTGGAAGAGGTACT  960
300   W  V  V  P  A  N  K  Q  I  N  S  F  Q  V  F  V  E  E  V  L   319

961  GAAAATCGCTCTGAGCGATGGCTTCTGCATCGATTCTTCTCACCCACATGCTCTGGATTT  1020
320   K  I  A  L  S  D  G  F  C  I  D  S  S  H  P  H  A  L  D  F   339

1021 TATGAACAATAAGATTATTCGATTAATACGGTACAGGTAAAAGGACCCCAACAACACTGG  1080
340   M  N  N  K  I  I  R  L  I  R  Y  R                          351

1081 AGATGGGGAGTCCCAGGAAGCTCATGTCAGCCAGGTCTTGGAGGGCATCTCGCCAGTGGT  1140

1141 GCGAGGCAGGGGACTATACTAATCTGTATTAATTGTGTAGCAGGACTTGATTCCCCCCAT  1200

1201 GATGAAGTCCACCTTTTGGAATCCAGTGTCCTCTGAACAGAACCACCTTTTTTCTTGCCA  1260

1261 TTTTGAGCTGCAGACAGGCGGTTTATTATGACAAGTGAAGAGTCAGCTGATGTGTACTAA  1320

1321 AGGAGGCCATAGGAGGATTTTCCAGCCAGGACAAAAGAGCAGCAGTTTTCTCCTGGGCTC  1380

1381 CATCTCTCTGTACCGCTAGCCAGTGCCGCATTTATCCATCTGTAAGAAGGCCCTGGTGGA  1440

1441 GAGGATGGGATGAGAACAAGAGGCTACCTCCAGTTAACCAGGACATAAAGTCCCCAGCGG  1500

1501 TTCCTGTCACACCTGCTCCTCCCTCCCCAGGGTGCATCCATGATCGTGGATGTTTGCCCA  1560

1561 GGGGTGACCATGTTTGGCTGGCTTGGAATGCTGTGCATTCTCAGAGCTCTGTTAGTGTCC  1620

1621 CCTCTTGGGGGTCAGAGATGAGGTGTGGCAGGGTCTAGAGGAATGAGTGTCCAGGCAGAG  1680

1681 TTCAGAAGGTAGGAATGTCCCTCTTGATAGGGCTGAATCAAGGGATTCCTGGCTTTAGAA  1740

1741 AGGGTCTGCTATCTTTGCAAAAATGTGCAAGTATCTGTAGCCAGTGTAATGAAATCACTT  1800

1801 CCAAATCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  1839
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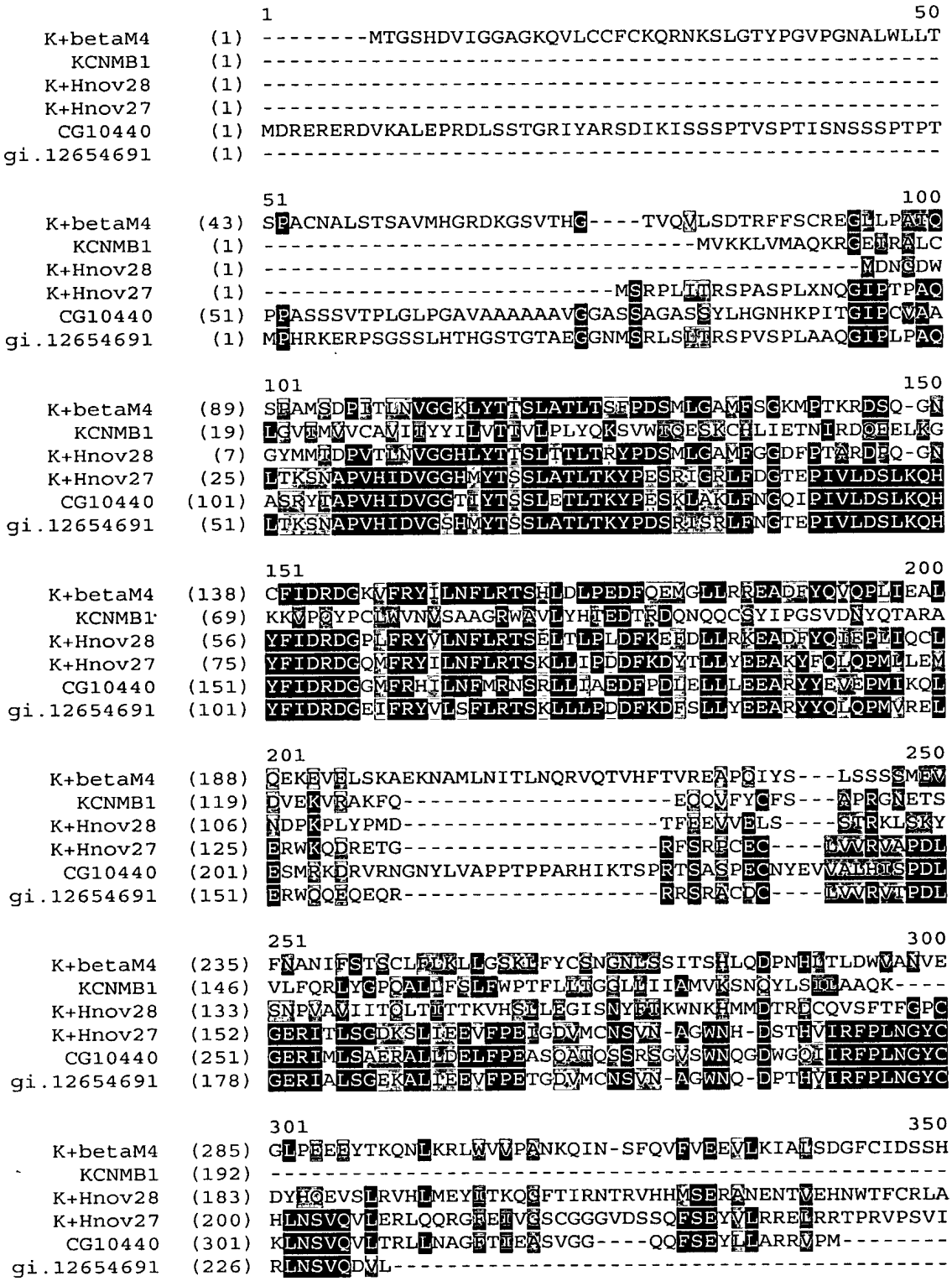
Figure 2A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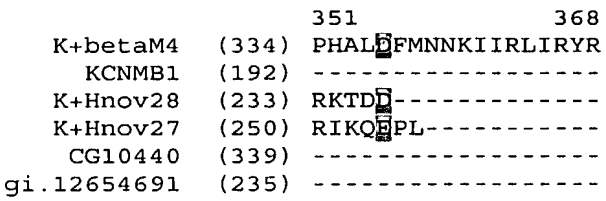
K+betaM4 (1) --------MTGSHDVIGGAGKQVLCCFCKQRNKSLGTYPGVPGNALWLLT
KCNMB1 (1) ----------
K+Hnov28 (1) ----------
K+Hnov27 (1) ----------
CG10440 (1) MDRERERDVKALEPRDLSSTGRIYARSDIKISSSPTVSPTISNSSSPTPT
gi.12654691 (1) ----------
51 100
K+betaM4 (43) SPACNALSTSAVMHGRDKGSVTHG----TVQVLSDTRFFSCREGLLPAAQ
KCNMB1 (1) ----------MVKKLVMAQKRGEIRALC
K+Hnov28 (1) ----------MDNGDW
K+Hnov27 (1) ----------MSRPLIIRSPASPLXNQGIPTPAQ
CG10440 (51) PPASSSVTPLGLPGAVAAAAAAVGGASSAGASSYLHGNHKPITGIPCVAA
gi.12654691 (1) MPHRKERPSGSSLHTHGSTGTAEGGNMSRLSITRSPVSPLAAQGIPLPAQ
101 150
K+betaM4 (89) SPAMSDPITTLNVGGKLYTTSLATLTSFPDSMLGAMFSGKMPTKRDSQ-GN
KCNMB1 (19) LGVTMVVCAVITYYILVTTVLPLYQKSVWTQESKCHLIETNIRDQFELKG
K+Hnov28 (7) GYMMTDPVTLNVGGHLYTTSLTTLTRYPDSMLGAMFGGDFPTARDFQ-GN
K+Hnov27 (25) LTKSNAPVHIDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQH
CG10440 (101) ASRYTAPVHIDVGGTIYTSSLETLTKYPESKLAKLFNGQIPIVLDSLKQH
gi.12654691 (51) LTKSNAPVHIDVGSHMYTSSLATLTKYPDSRITSRLFNGTEPIVLDSLKQH
151 200
K+betaM4 (138) CFIDRDGKVFRYILNFLRTSHLDLPEDFQEMGLLRREADFYQVQPLIEAL
KCNMB1 (69) KKVPQYPCLWVNVSAAGRWAVLYHIEDTRDQNQQCSYIPGSVDNYQTARA
K+Hnov28 (56) YFIDRDGPLFRYVLNFLRTSELTLPLDFKEFDLLRKEADFYQIEPLIQCL
K+Hnov27 (75) YFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQLQPMLLEM
CG10440 (151) YFIDRDGGMFRHILNFMRNSRLLIAEDFPDIELLLEEARYYEVEPMIKQL
gi.12654691 (101) YFIDRDGEIFRYVLSFLRTSKLLLPDDFKDFSLLYEEARYYQLQPMVREL
201 250
K+betaM4 (188) QEKEVELSKAEKNAMLNITLNQRVQTVHFTVREAPQIYS---LSSSSMEV
KCNMB1 (119) DVEKVRAKFQ----------EQQVFYCFS---APRGNETS
K+Hnov28 (106) NDPKPLYPMD----------TFEEVVELS----STRKLSKY
K+Hnov27 (125) ERWKQDRETG----------RFSRECEC----LVVRVAPDL
CG10440 (201) ESMRKDRVRNGNYLVAPPTPPARHIKTSPRTSASPECNYEVVALHTSPDL
gi.12654691 (151) ERWQQEQEQR----------RRSRACDC----LVVRVTPDL
251 300
K+betaM4 (235) FNANIFSTSCLFDKLLGSKLFYCSNGNLSSITSHLQDPNHLTLDWVANVE
KCNMB1 (146) VLFQRLYGPQALIFSLFWPTFLVTGGLLIIAMVKSNQYLSDLAAQK----
K+Hnov28 (133) SNPVAVIITQLTITTKVHSTLEGISNYFTKWNKFMMDTRDCQVSFTFGPC
K+Hnov27 (152) GERITLSGDKSLIEEVFPEIGDVMCNSVN-AGWNH-DSTHVIRFPLNGYC
CG10440 (251) GERIMLSAERALLDELFPEASQATQSSRSGVSWNQGDWGQIIRFPLNGYC
gi.12654691 (178) GERIALSGEKALIEEVFPETGDVMCNSVN-AGWNQ-DPTHYIRFPLNGYC
301 350
K+betaM4 (285) GLPEEEYTKQNLKRLWVVPANKQIN-SFQVFVEEVLKIALSDGFCIDSSH
KCNMB1 (192) ----------
K+Hnov28 (183) DYHQEVSLRVHLMEYITKQSFTIRNTRVHHMSERANENTVEHNWTFCRLA
K+Hnov27 (200) HLNSVQVLERLQQRGFEIVGSCGGGVDSSQFSEYVLRREIRRTPRVPSVI
CG10440 (301) KLNSVQVLTRLLNAGFTIEASVGG----QQFSEYLLARRVPM--------
gi.12654691 (226) RLNSVQDVL----------

Figure 2B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368
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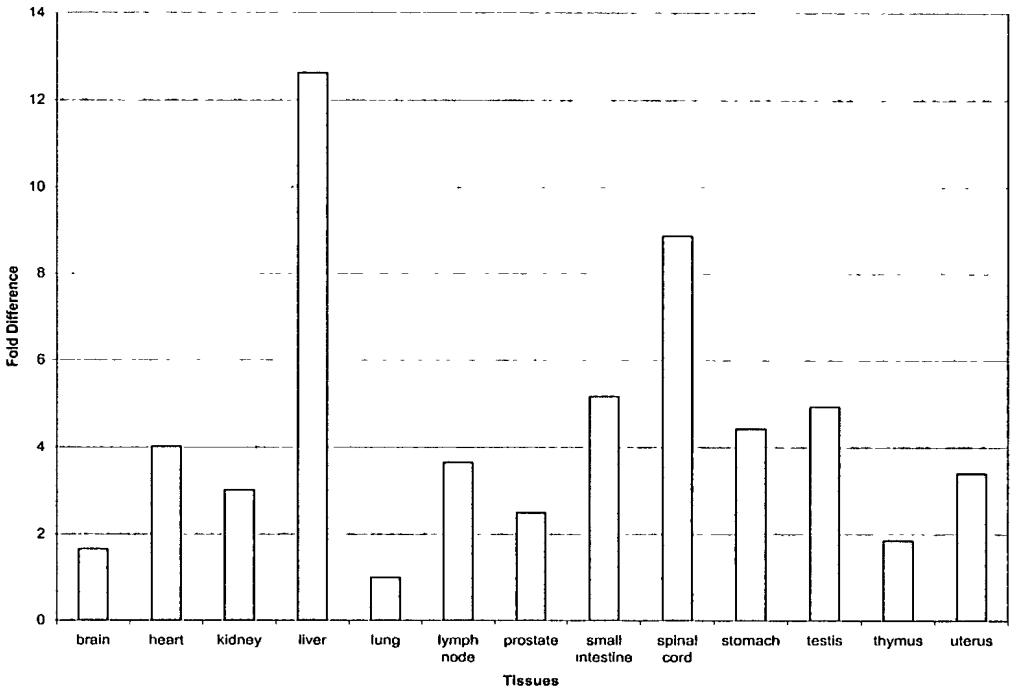
KCNMB1 (192) ----------
K+Hnov28 (233) RKTDD----------
K+Hnov27 (250) RIKQEPL----------
CG10440 (339) ----------
gi.12654691 (235) ----------

Figure 3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12
10
8
6
4
2
0
Fold Difference
brain
heart
kidney
liver
lung
lymph node
prostate
small intestine
spinal cord
stomach
testis
thymus
uterus
Tissues

D0115 NP

Figure 4.

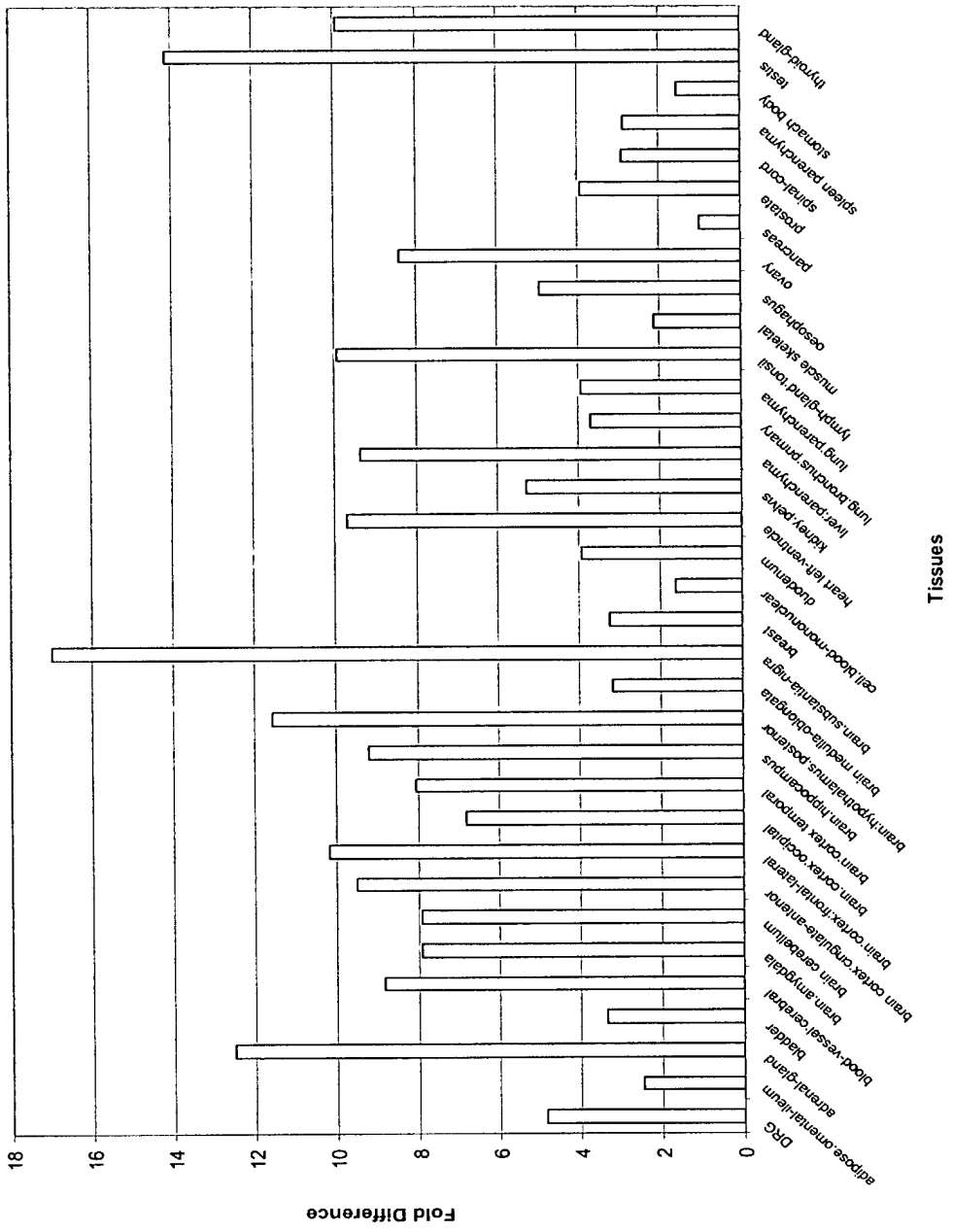
K+betaM4

Protein	Genbank ID	Identities	Similarities
human potassium channel K+Hnov27 protein	gi| Y34125	31.6%	45.1%
human potassium channel K+Hnov28 protein	gi| Y34129	42.3%	50.5%
human neuroblastoma protein	gi|12654691	36.2%	47.3%
Drosophila CG10440 protein	gi|7291303	28.0%	38.6%
Human Maxi-K potassium channel beta subunit, KCNMB1	gi|4758625	26.1%	39.1%

K+betaM5

Protein	Genbank ID	Identities	Similarities
human potassium channel K+Hnov28 protein	gi| Y34129	31.7%	43.4%
the human lung protein, MGC:2376	gi|12654469	34.4%	45.6%
human MSTP028 protein	gi|11640564	31.7%	43.4%
Caenorhabditis K+ channel tetramerisation domain containing protein	gi|3875362	34.4%	45.6%
Drosophila CG10465 protein	gi|7302243	30.8%	38.3%
Human Maxi-K potassium channel beta subunit, KCNMB1	gi|4758625	20.0%	40.0%

Figure 5


Fold Difference
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2
4
6
8
10
12
14
16
18
Tissues
adipose omentab-ileum
DRG
adrenal-gland
bladder
blood-vessel cerebral
brain amygdala
brain cerebellum
brain cortex cingulate-anterior
brain cortex frontal-anterior
brain cortex occipital
brain cortex temporal
brain hippocampus
brain hypothalamus posterior
brain medulla-oblongata
brain substantia-nigra
breast
cell blood-mononuclear
duodenum
heart left-ventricle
kidney pelvis
liver parenchyma
lung bronchus primary
lung parenchyma
lymph-gland tonsil
muscle skeletal
oesophagus
ovary
pancreas
prostate
spina-cord
spleen parenchyma
stomach body
testis
thyroid-gland

Figure 6A

```
   1  ATGACGATGGCGGTTTTGCGGAATAGAAAAGGGGGAAAGGGACCACTCAGGCGCCGGCCG   60
   1  M  T  M  A  V  L  R  N  R  K  G  G  K  G  P  L  R  R  R  P    20

  61  CTGGCGCTGCCTGCTCTTCGACTGGGCGAGCTTCCTGCCAATCAGGGCGGAACCAGCGCG  120
  21  L  A  L  P  A  L  R  L  G  E  L  P  A  N  Q  G  G  T  S  A    40

 121  GCGTCGGCCAGTAGCGGGAGGCGGTCGGGTCAGGCCCCAGCTGGGCGCGAGCGGGTCGGC  180
  41  A  S  A  S  S  G  R  R  S  G  Q  A  P  A  G  R  E  R  V  G    60

 181  GTTGAGGGAGCCACCGCCCTCCCGCCTGCGCACTGCCTCTCGCCCCCCTCCGGCCAGCCC  240
  61  V  E  G  A  T  A  L  P  P  A  H  C  L  S  P  P  S  G  Q  P    80

 241  GCAGCCGGCCGCGTCATGCCAGGCGCTGCTCGGCGAGCCAGAGGGATGGTGGTAGTCACG  300
  81  A  A  G  R  V  M  P  G  A  A  R  R  A  R  G  M  V  V  V  T   100

 301  GGGCGGGAGCCAGACAGCCGTCGTCAGGACGGTGCCATGTCCAGCTCTGACGCCGAAGAC  360
 101  G  R  E  P  D  S  R  R  Q  D  G  A  M  S  S  S  D  A  E  D   120

 361  GACTTTCTGGAGCCGGCCACGCCGACGGCCACGCAGGCGGGGCACGCGCTGCCCCTGCTG  420
 121  D  F  L  E  P  A  T  P  T  A  T  Q  A  G  H  A  L  P  L  L   140

 421  CCACAGGAGTTTCCTGAGGTTGTTCCCCTTAACATCGGAGGGGCTCACTTCACTACACGC  480
 141  P  Q  E  F  P  E  V  V  P  L  N  I  G  G  A  H  F  T  T  R   160

 481  CTGTCCACACTGCGGTGCTACGAAGACACCATGTTGGCAGCCATGTTCAGTGGGCGGCAC  540
 161  L  S  T  L  R  C  Y  E  D  T  M  L  A  A  M  F  S  G  R  H   180

 541  TACATCCCCACAGACTCCGAGGGCCGGTACTTCATCGACCGAGATGGCACACACTTTGGA  600
 181  Y  I  P  T  D  S  E  G  R  Y  F  I  D  R  D  G  T  H  F  G   200

 601  GATGTGCTGAATTTCCTGCGCTCAGGGGACCTCCCACCCAGGGAGCGTGTTCGAGCTGTG  660
 201  D  V  L  N  F  L  R  S  G  D  L  P  P  R  E  R  V  R  A  V   220

 661  TACAAAGAGGCCCAGTACTATGCCATCGGGCCCCTCCTGGAGCAGCTGGAGAACATGCAG  720
 221  Y  K  E  A  Q  Y  Y  A  I  G  P  L  L  E  Q  L  E  N  M  Q   240

 721  CCACTGAAGGGCGAGAAGGTGCGCCAAGCGTTTCTGGGACTCATGCCCTATTACAAAGAC  780
 241  P  L  K  G  E  K  V  R  Q  A  F  L  G  L  M  P  Y  Y  K  D   260

 781  CACTTGGAGCGGATTGTGGAGATCGCCCGGCTGCGTGCGGTCCAGCGGAAGGCCCGCTTT  840
 261  H  L  E  R  I  V  E  I  A  R  L  R  A  V  Q  R  K  A  R  F   280
```

Figure 6B

```
841  GCCAAGCTCAAGAGCTTGACACCTTCCTGGCTAATGAGTGTCCTCATCAAGATGCCCCCT  900
281  A  K  L  K  S  L  T  P  S  W  L  M  S  V  L  I  K  M  P  P    300

901  GGAGTCACATCATGGATTAACGCAGAAAGGCGGCTGTATTTGGAAACTCCCATTGGTCCA  960
301  G  V  T  S  W  I  N  A  E  R  R  L  Y  L  E  T  P  I  G  P    320

961  GAGAGACAGAACAATGAGAAGAAATCCCCTGTCCAGTTGCCTGCAGGAGTATTCCAACAC  1020
321  E  R  Q  N  N  E  K  K  S  P  V  Q  L  P  A  G  V  F  Q  H    340

1021 TTCATGGGCTAGAGGATTCCATTGAGATGGGGTTTACGTCTTGATTTTGAACACCTGTCA  1080
341  F  M  G                                                       343

1081 GCACTGTTCTCTGTTTGCATGGCAATTCTGACCCTTTTATGGCAACAACACCCCTGGGAC  1140

1141 AACCCAGATTTGTAGATTGAGATCCAAAGGTAGAATTTCCAGACAGTCCAACCAAGGTAT  1200

1201 CAAGTGATGTTTCCAGAGTGGAAGGCTCTCACCGTGTCCCAGGATTTCTGGGGTTTGTAA  1260

1261 GCAGTACTGGCCATTTGTGACCCTGTTTTTTACCTAATCATTCTGTCTTTTTAGGACATG  1320

1321 GTTTTACCCGATCCCTGGCAAAGGATCCAGAATTCCAATAGCTGAAAACCCTGTTATAGC  1380

1381 TTTTCTCCTATTCTGCCTTACCCAAGACACACTTGAACCCCTCAGTAAGGCTATAGAGAG  1440

1441 GGCCATGAGCAGGGGCAGCCTCTCCCTTGTTTCTACAGCTCCATGATGAGGGGTTGACTG  1500

1501 AGGCCAGCAATCCTTGTAGGTGTGACAGTTGCAATATAATTAACAGTTTCAAGATCTAGA  1560

1561 GGTACCTTTTGAAAGAACCCCTTCAGGGATATCTATCCACAGTAGCCTGGAGCAGCCAAG  1620

1621 GTGAACCTGAGATTTTGACCCACACAATAAGGGGGGGCCATTCTTTTTCAAATATTTTGG  1680

1681 CTTCAGAATACACTTCATTACACATGCAAATATTGAGAGATTAACAGAAATTCCAGCTCT  1740

1741 TATGCCTAACTGAGAAGAGCCACTGCAAGTTGCAGTTAGGTACCCATGTGCAGCAGAGGC  1800

1801 CAGCTGAATCCCAGAGCTTCCCAAAGTGGACACCAGCGGGGACTATTCCTGATGTCCCAC  1860

1861 CCAAGAGAGGAAGATGAGCTGAGGCGCTCTTGCTCTGCCCAAATGCATCCCATGTGCATT  1920
```

Figure 6C

```
1921  CACGTGTCACCCATTCAAAATAACATGGCATTCTTGGAACCTTGTATCTGACATGTAAGA  1980

1981  CCAGCCTACACATTGGGGTGGGTGCAGGGGCTCACACTTGTAATCCTAGCACTTTGGAAG  2040

2041  GCTGAGGTGGGCAGATTGCTTGAGCACAGGAGTTCCAGACCAGCCTGAGCAACATGGCGA  2100

2101  AATCCTGTCTCTTCAAGAAATAAAATAATAATAATAATAAAAAAAAAAAAAAAA  2154
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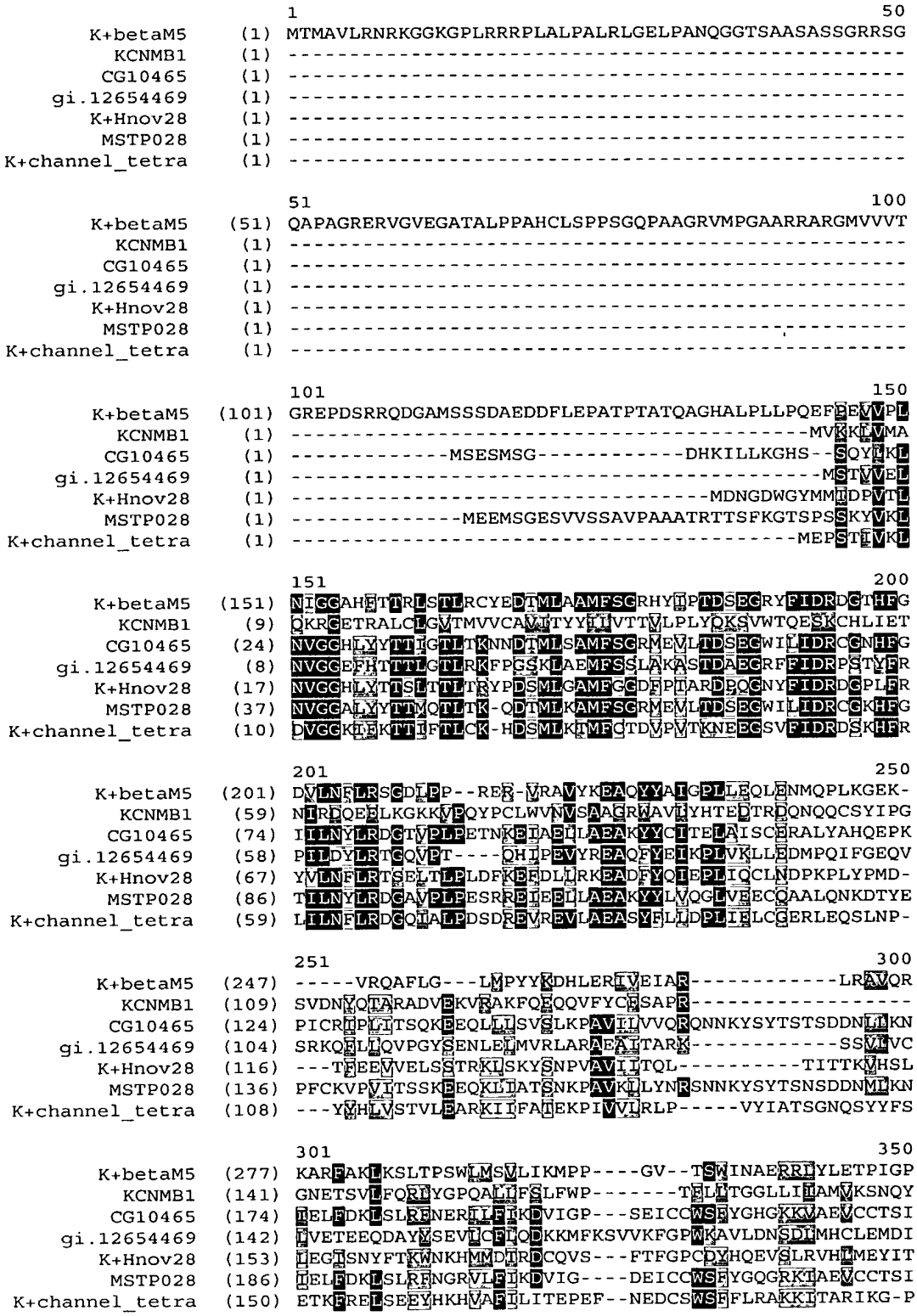
Figure 7A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KCNMB1 (1)
CG10465 (1)
gi.12654469 (1)
K+Hnov28 (1)
MSTP028 (1)
K+channel_tetra (1)
51 100
K+betaM5 (51) QAPAGRERVGVEGATALPPAHCLSPPSGQPAAGRVMPGAARRARGMVVVT
KCNMB1 (1)
CG10465 (1)
gi.12654469 (1)
K+Hnov28 (1)
MSTP028 (1)
K+channel_tetra (1)
101 150
K+betaM5 (101) GREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHALPLLPQEFPEVVPL
KCNMB1 (1) MVKKLVMA
CG10465 (1) MSESMSG DHKILLKGHS SQYLKL
gi.12654469 (1) MSTVVEL
K+Hnov28 (1) MDNGDWGYMMIDPVTL
MSTP028 (1) MEEMSGESVVSSAVPAAATRTTSFKGTSPSSKYVKL
K+channel_tetra (1) MEPSTIVKL
151 200
K+betaM5 (151) NIGGAHETTRLSTLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFG
KCNMB1 (9) QKRGETRALCLGVTMVVCAVITYYIIVTTVLPLYQKSVWTQESKCHLIET
CG10465 (24) NVGGHLYYTTIGTLTKNNDTMLSAMFSGRMEVLTDSEGWILIDRCGNHFG
gi.12654469 (8) NVGGEFHTTTLGTLRKFPGSKLAEMFSSLAKASTDAEGRFFIDRPSTYFR
K+Hnov28 (17) NVGGHLYTTSLTTLTRYPDSMLGAMFGGDFPTARDPQGNYFIDRDGPLFR
MSTP028 (37) NVGGALYYTTMQTLTK-QDTMLKAMFSGRMEVLTDSEGWILIDRCGKHFG
K+channel_tetra (10) DVGGKHEKTTIFTLCK-HDSMLKTMFCTDVPVTKNEEGSVFIDRDSKHFR
201 250
K+betaM5 (201) DVLNFLRSGDLPP--RER-VRAVYKEAQYYAIGPLLEQLENMQPLKGEK-
KCNMB1 (59) NIRDQEELKGKKVPQYPCLWVNVSAAGRWAVIYHTEDTRDQNQQCSYIPG
CG10465 (74) IILNYLRDGTVPLPETNKEIAELLAEAKYYCITELAISCERALYAHQEPK
gi.12654469 (58) PILDYLRTGQVPT----QHIPEVYREAQFYEIKPLVKLLEDMPQIFGEQV
K+Hnov28 (67) YVLNFLRTSELTLPLDFKEEDLLRKEADFYQIEPLIQCLNDPKPLYPMD-
MSTP028 (86) TILNYLRDGAVPLPESRREIEELLAEAKYYLVQGLVEECQAALQNKDTYE
K+channel_tetra (59) LILNFLRDGQIALPDSDREVREVLAEASYFLLDPLIELCGERLEQSLNP-
251 300
K+betaM5 (247) -----VRQAFLG---LMPYYKDHLERIVEIAR----------LRAVQR
KCNMB1 (109) SVDNYQTARADVEKVRAKFQEQQVFYCESAPR----------
CG10465 (124) PICRIPLITSQKEEQLLLSVSLKPAVILVVQRQNNKYSYTSTSDDNLLKN
gi.12654469 (104) SRKQELLQVPGYSENLELMVRLARAEAITARK----------SSVLVC
K+Hnov28 (116) ---TFEEVVELSSTRKLSKYSNPVAVILTQL----------TITTKVHSL
MSTP028 (136) PFCKVPVITSSKEEQKLIATSNKPAVKLLYNRSNNKYSYTSNSDDNMLKN
K+channel_tetra (108) ---YVHLVSTVLEARKIIFAIEKPIVVLRLP-----VYIATSGNQSYYFS
301 350
K+betaM5 (277) KARFAKLKSLTPSWLMSVLIKMPP----GV--TSWINAERRILYLETPIGP
KCNMB1 (141) GNETSVLFQRIYGPQALIFSLFWP-------TELLTGGLLIIIAMVKSNQY
CG10465 (174) IELFDKLSLRENERIIFIKDVIGP---SEICCWSFYGHGKKVAEVCCTSI
gi.12654469 (142) IVETEEQDAYVSEVLCFLQDKKMFKSVVKFGPWKAVLDNSDIMHCLEMDI
K+Hnov28 (153) IEGISNYFTKWNKHMMDIRDCQVS---FTFGPCDYHQEVSLRVHLMEYIT
MSTP028 (186) IELFDKLSLRFNGRVLEIKDVIG----DEICCWSFYGQGRKIAEVCCTSI
K+channel_tetra (150) ETKFRELSEEYHKHVAFILITEPEF--NEDCSWSFFLRAKKITARIKG-P

Figure 7B

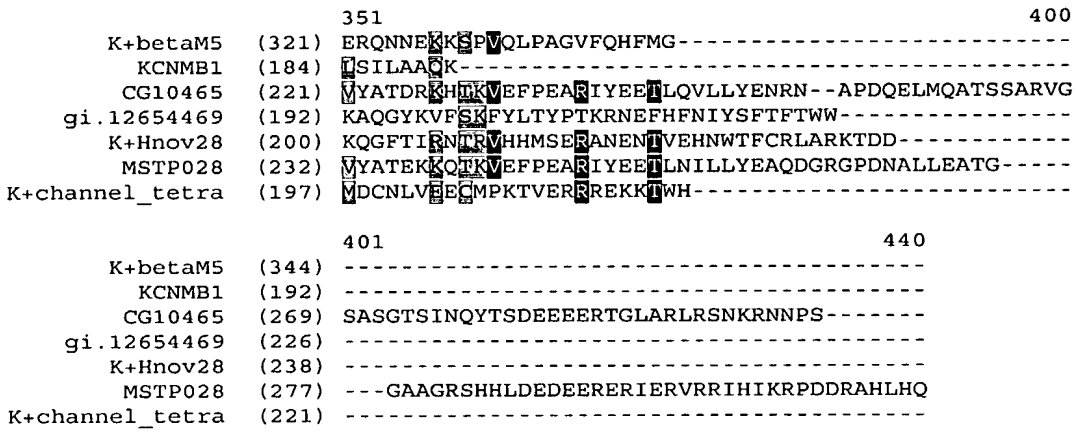

351
400
K+betaM5 (321) ERQNNEKKSPVQLPAGVFQHFMG----------
KCNMB1 (184) TSILAAQK----------
CG10465 (221) VYATDRKHIKVEFPEARIYEETLQVLLYENRN--APDQELMQATSSARVG
gi.12654469 (192) KAQGYKVFSKFYLTYPTKRNEFHFNIYSFTFTWW----------
K+Hnov28 (200) KQGFTIRNTRVHHMSERANENTVEHNWTFCRLARKTDD----------
MSTP028 (232) VYATEKKQTKVEFPEARIYEETLNILLYEAQDGRGPDNALLEATG-----
K+channel_tetra (197) MDCNLVEECMPKTVERRREKKTWH----------
401
440
K+betaM5 (344) ----------
KCNMB1 (192) ----------
CG10465 (269) SASGTSINQYTSDEEEERTGLARLRSNKRNNPS-------
gi.12654469 (226) ----------
K+Hnov28 (238) ----------
MSTP028 (277) ---GAAGRSHHLDEDEERERIERVRRIHIKRPDDRAHLHQ
K+channel_tetra (221) ----------

Figure 8

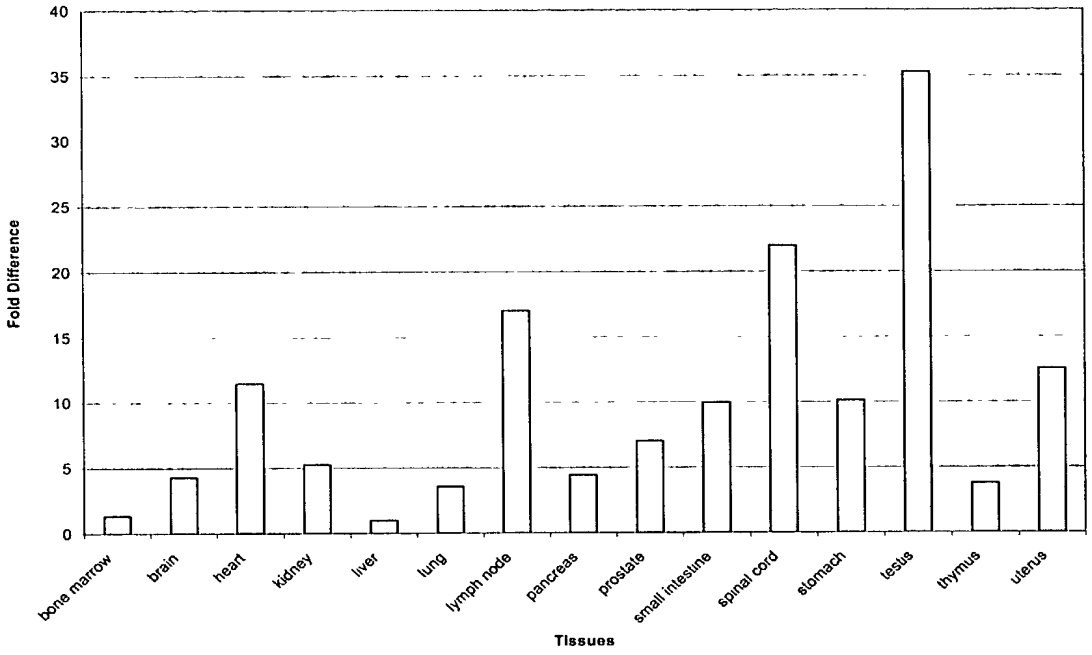
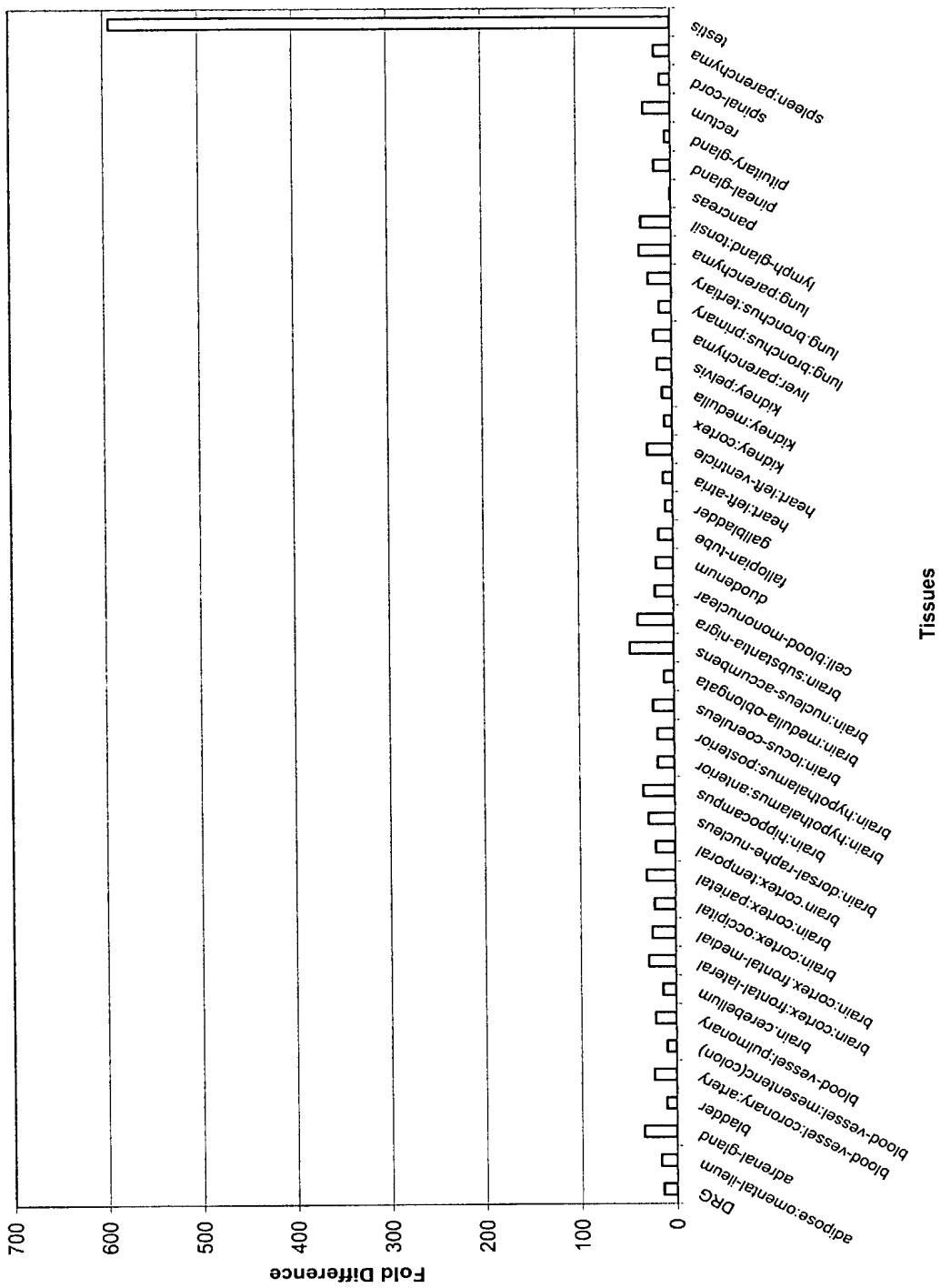

40
35
30
25
20
15
10
5
0
Fold Difference
bone marrow
brain
heart
kidney
liver
lung
lymph node
pancreas
prostate
small intestine
spinal cord
stomach
testis
thymus
uterus
Tissues

Figure 9


Fold Difference
700
600
500
400
300
200
100
0
Tissues
DRG
adipose:omental-ileum
adrenal-gland
bladder
blood-vessel:coronary:artery
blood-vessel:mesenteric(colon)
blood-vessel:pulmonary
brain:cerebellum
brain:cortex:frontal-lateral
brain:cortex:frontal-medial
brain:cortex:occipital
brain:cortex:parietal
brain:cortex:temporal
brain:dorsal-raphe-nucleus
brain:hippocampus
brain:hypothalamus:anterior
brain:hypothalamus:posterior
brain:locus-coeruleus
brain:medulla-oblongata
brain:nucleus-accumbens
brain:substantia-nigra
cell:blood-mononuclear
duodenum
fallopian-tube
gallbladder
heart:left-atria
heart:left-ventricle
kidney:cortex
kidney:medulla
kidney:pelvis
liver:parenchyma
lung:bronchus:primary
lung:bronchus:tertiary
lung:parenchyma
lymph-gland:tonsil
pancreas
pineal-gland
pituitary-gland
rectum
spinal-cord
spleen:parenchyma
testis